

Serial Number: 07/371, 333A

ENTERED



Changed a file from non-ASCII to ASCII



Changed the margins in cases where the sequence text was "wrapped" down to the next line.



Edited a format error in the Current Application Data section, specifically:

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other

Added the mandatory heading and subheadings for "Current Application Data".



Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.



Changed the spelling of a mandatory field (the headings or subheadings), specifically:



Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:



Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:



Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.



Inserted colons after headings/subheadings. Headings edited included:



Deleted extra, invalid, headings used by an applicant, specifically:

Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as

Inserted mandatory headings, specifically:



Corrected an obvious error in the response, specifically:



Edited identifiers where upper case is used but lower case is required, or vice versa.



Corrected an error in the Number of Sequences field, specifically:



A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected:

Other:

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

1646

RAW SEQUENCE LISTING                      DATE: 03/05/2001  
 PATENT APPLICATION: US/09/371,333A      TIME: 14:42:25

Input Set : A:\Pto.vsk  
 Output Set: N:\CRF3\03052001\I371333A.raw

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3 <110> APPLICANT: Xu, Wenfeng
4   Presnell, Scott R.
5   Yee, David P.
6   Foster, Donald C.
8 <120> TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR PARA
9   (ZCHEMR2)
11 <130> FILE REFERENCE: 98-10D1
13 <140> CURRENT APPLICATION NUMBER: US 09/371,333A
14 <141> CURRENT FILING DATE: 1999-08-10
16 <150> PRIOR APPLICATION NUMBER: US 09/053,866
17 <151> PRIOR FILING DATE: 1998-04-01
19 <160> NUMBER OF SEQ ID NOS: 21
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 4895
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (176)...(1330)
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35   ggtccggcga ggcaggaagc ctgaggccac agcccagagc agcctgagtg cagtc atg   178
36                                     Met
37                                     1
39   tgg ggg cga ctg ctc ctg tgg ccc ctg gty ctg ggg ttc agc ctg tct   226
40   Trp Gly Arg Leu Leu Leu Trp Pro Leu Val Leu Gly Phe Ser Leu Ser
41       5                10                15
43   ggc ggc acc cag acc ccc agc gtc tac gac gag agc ggg agc acc gga   274
44   Gly Gly Thr Gln Thr Pro Ser Val Tyr Asp Glu Ser Gly Ser Thr Gly
45       20                25                30
47   ggt ggt gat gac agc acg ccc tca atc ctg cct gcc ccc cgc ggc tac   322
48   Gly Gly Asp Asp Ser Thr Pro Ser Ile Leu Pro Ala Pro Arg Gly Tyr
49       35                40                45
51   cca ggc caa gtc tgt gcc aat gac agt gac acc ctg gag ctc ccg gac   370
52   Pro Gly Gln Val Cys Ala Asn Asp Ser Asp Thr Leu Glu Leu Pro Asp
53       50                55                60                65
55   agc tca cgg gca ctg ctt ctg ggc tgg gty ccc acc agg ctg gty ccc   418
56   Ser Ser Arg Ala Leu Leu Gly Trp Val Pro Thr Arg Leu Val Pro
57       70                75                80
59   gcc ctc tat ggg ctg gtc ctg gty gty ggg ctg ccg gcc aat ggg ctg   466
60   Ala Leu Tyr Gly Leu Val Leu Val Val Gly Leu Pro Ala Asn Gly Leu
61       85                90                95
63   gcg ctg tgg gty ctg gcc acg cag gca cct cgg ctg ccc tcc acc atg   514
64   Ala Leu Trp Val Leu Ala Thr Gln Ala Pro Arg Leu Pro Ser Thr Met
65       100               105               110

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67	ctg	ctg	atg	aac	ctc	gcg	act	gct	gac	ctc	ctg	ctg	gcc	ctg	gcg	ctg	562
68	Leu	Leu	Met	Asn	Leu	Ala	Thr	Ala	Asp	Leu	Leu	Leu	Ala	Leu	Ala	Leu	
69		115				120					125						
71	ccc	ccg	cgg	atc	gcc	tac	cac	ctg	cgt	ggc	cag	cgc	tgg	ccc	ttc	ggg	610
72	Pro	Pro	Arg	Ile	Ala	Tyr	His	Leu	Arg	Gly	Gln	Arg	Trp	Pro	Phe	Gly	
73	130				135					140					145		
75	gag	gcc	gcc	tgc	cgc	ctg	gcc	acg	gcc	gca	ctc	tat	ggg	cac	atg	tat	658
76	Glu	Ala	Ala	Cys	Arg	Leu	Ala	Thr	Ala	Ala	Leu	Tyr	Gly	His	Met	Tyr	
77				150					155					160			
79	ggc	tca	gtg	ctg	ctg	ctg	gcc	gcc	gtc	agc	ctg	gat	cgc	tac	ctg	gcc	706
80	Gly	Ser	Val	Leu	Leu	Leu	Ala	Ala	Val	Ser	Leu	Asp	Arg	Tyr	Leu	Ala	
81				165					170					175			
83	ctg	gtg	cac	ccg	ctg	cgg	gcc	cgc	gcc	ctg	cgt	ggc	cgg	cgc	ctg	gcc	754
84	Leu	Val	His	Pro	Leu	Arg	Ala	Arg	Ala	Leu	Arg	Gly	Arg	Arg	Leu	Ala	
85			180					185					190				
87	ctt	gga	ctc	tgc	atg	gct	gct	tgg	ctc	atg	gcg	gcc	gcc	ctg	gca	ctg	802
88	Leu	Gly	Leu	Cys	Met	Ala	Ala	Trp	Leu	Met	Ala	Ala	Ala	Leu	Ala	Leu	
89			195					200					205				
91	ccc	ctg	aca	ctg	cag	cgg	cag	acc	ttc	cgg	ctg	gcg	cgc	tcc	gat	cgc	850
92	Pro	Leu	Thr	Leu	Gln	Arg	Gln	Thr	Phe	Arg	Leu	Ala	Arg	Ser	Asp	Arg	
93	210					215						220			225		
95	gtg	ctc	tgc	cat	gac	gcg	ctg	ccc	ctg	gac	gca	cag	gcc	tcc	cac	tgg	898
96	Val	Leu	Cys	His	Asp	Ala	Leu	Pro	Leu	Asp	Ala	Gln	Ala	Ser	His	Trp	
97				230						235					240		
99	caa	ccg	gcc	ttc	acc	tgc	ctg	gcg	ctg	ttg	ggc	tgt	ttc	ctg	ccc	ctg	946
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101			245						250					255			
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104	Leu	Ala	Met	Leu	Leu	Cys	Tyr	Gly	Ala	Thr	Leu	His	Thr	Leu	Ala	Ala	
105			260					265					270				
106	agc	ggc	cgg	cgc	tac	ggc	cac	gcg	ctg	agg	ctg	acc	gca	gtg	gtg	ctg	1042
107	Ser	Gly	Arg	Arg	Tyr	Gly	His	Ala	Leu	Arg	Leu	Thr	Ala	Val	Val	Leu	
108			275					280					285				
110	gcc	tcc	gcc	gtg	gcc	ttc	ttc	gtg	ccc	agc	aac	ctg	ctg	ctg	ctg	ctg	1090
111	Ala	Ser	Ala	Val	Ala	Phe	Phe	Val	Pro	Ser	Asn	Leu	Leu	Leu	Leu	Leu	
112			290			295					300				305		
114	cat	tac	tcg	gac	ccg	agc	ccc	agc	gcc	tgg	ggc	aac	ctc	tat	ggg	gcc	1138
115	His	Tyr	Ser	Asp	Pro	Ser	Pro	Ser	Ala	Trp	Gly	Asn	Leu	Tyr	Gly	Ala	
116				310					315					320			
118	tac	gtg	ccc	agc	ctg	gcg	ctg	agc	acc	ctc	aac	agc	tgc	gtg	gat	ccc	1186
119	Tyr	Val	Pro	Ser	Leu	Ala	Leu	Ser	Thr	Leu	Asn	Ser	Cys	Val	Asp	Pro	
120				325					330					335			
122	ttc	atc	tac	tac	gtg	tcg	gcc	gag	ttc	agg	gac	aag	gtg	cgg	gca		1234
123	Phe	Ile	Tyr	Tyr	Tyr	Val	Ser	Ala	Glu	Phe	Arg	Asp	Lys	Val	Arg	Ala	
124			340					345					350				
126	ggg	ctc	ttc	caa	cgg	tcg	ccg	ggg	gac	acc	gtg	gcc	tcc	aag	gcc	tct	1282
127	Gly	Leu	Phe	Gln	Arg	Ser	Pro	Gly	Asp	Thr	Val	Ala	Ser	Lys	Ala	Ser	
128			355					360					365				
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132	370				375				380					385			
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135	cttcctggga	cctcagaatg	tgaccttatt	tgaaaatagg	gttggtacaa	ctgtcactag											1450
136	cggaggtcac	tttgagaaag	ggtgggcctt	acatccagtg	tggtgtgtgt	cctcataaga											1510
137	taagygaggg	ccaggcctgg	tggtcacgc	ctgtaatccc	agcactttaa	gaggccaagg											1570
138	cggatggatc	acttgagccc	aggagttcaa	caccagcctg	agcaacatyg	laaaacccca											1630
139	tctctaccaa	aaatacaaaa	attagctggg	cttggtggct	ggcgccctga	atcccagcta											1690
140	ctcaggagac	tgaggcagaa	ggatcgcttg	aacctgggag	gcagaggttg	cagtgcgcg											1750
141	agattgcgcc	actggactcc	agcctgcgtg	acagagagcc	tgctctctaa	tttaattaat											1810
142	aaltaattta	attcaatttt	aaaaagacga	aaagtgacgg	ccaggtgcag	tggtcacgc											1870
143	ctataatctc	agcactctgg	gaggccaaga	tgaggattg	cttgaagcca	ggagtttggt											1930
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145	caggcattgt	ggcatgcgcc	tatagtccca	gccactcaag	aggcacaggg	gggaggatca											2050
146	cttgagccctg	ggaggttggt	gttgacgtga	gctatgattg	taccactgca	ctccagcctg											2110
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179	agtagtctga	cacggagact	ggcagcgccg	acgtcctgcc	caccacgcac	tcctcgagag											4090
180	cacggaaccg	cacgcacgtc	aggcaccggc	tggggatctg	tggggcaggc	gcgggcycag											4150

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182 gggataccca ggacgcgtga aacacagaag aaacgtgac ccattttctt tttttctttt 4270
183 acttttcttt tttttttttt ttcctgagac agagtctcgc gctgttgccc aggctggagt 4330
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188 acgtctcagg tggcctctga aacaccactc ctttttgggt gtgtgcacgc atggctgagc 4630
189 atgtgtgggt gggagtcagc acattcacga tactgtgcaa tcatcacctc tgtctagtta 4690
190 caggacgggt tctttctccc ccuaagaaac cccatcgcca tcagcactca ctccccactc 4750
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193 aaaaaaaaaa aaaaaaaaaa aaaaaa 4895
195 <210> SEQ ID NO: 2
196 <211> LENGTH: 385
197 <212> TYPE: PRT
198 <213> ORGANISM: Homo sapiens
200 <400> SEQUENCE: 2
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203 Ser Gly Gly Thr Gln Thr Pro Ser Val Tyr Asp Glu Ser Gly Ser Thr
204 20 25 30
206 Gly Gly Gly Asp Asp Ser Thr Pro Ser Ile Leu Pro Ala Pro Arg Gly
207 35 40 45
208 Tyr Pro Gly Gln Val Cys Ala Asn Asp Ser Asp Thr Leu Glu Leu Pro
209 50 55 60
210 Asp Ser Ser Arg Ala Leu Leu Leu Gly Trp Val Pro Thr Arg Leu Val
211 65 70 75 80
212 Pro Ala Leu Tyr Gly Leu Val Leu Val Val Gly Leu Pro Ala Asn Gly
213 85 90 95
214 Leu Ala Leu Trp Val Leu Ala Thr Gln Ala Pro Arg Leu Pro Ser Thr
215 100 105 110
216 Met Leu Leu Met Asn Leu Ala Thr Ala Asp Leu Leu Leu Ala Leu Ala
217 115 120 125
218 Leu Pro Pro Arg Ile Ala Tyr His Leu Arg Gly Gln Arg Trp Pro Phe
219 130 135 140
220 Gly Glu Ala Ala Cys Arg Leu Ala Thr Ala Ala Leu Tyr Gly His Met
221 145 150 155 160
222 Tyr Gly Ser Val Leu Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu
223 165 170 175
224 Ala Leu Val His Pro Leu Arg Ala Arg Ala Leu Arg Gly Arg Arg Leu
225 180 185 190
226 Ala Leu Gly Leu Cys Met Ala Ala Trp Leu Met Ala Ala Ala Leu Ala
227 195 200 205
228 Leu Pro Leu Thr Leu Gln Arg Gln Thr Phe Arg Leu Ala Arg Ser Asp
229 210 215 220
230 Arg Val Leu Cys His Asp Ala Leu Pro Leu Asp Ala Gln Ala Ser His
231 225 230 235 240
232 Trp Gln Pro Ala Phe Thr Cys Leu Ala Leu Leu Gly Cys Phe Leu Pro

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236 Ala Ser Gly Arg Arg Tyr Gly His Ala Leu Arg Leu Thr Ala Val Val
237           275           280           285
238 Leu Ala Ser Ala Val Ala Phe Phe Val Pro Ser Asn Leu Leu Leu Leu
239           290           295           300
240 Leu His Tyr Ser Asp Pro Ser Pro Ser Ala Trp Gly Asn Leu Tyr Gly
241           305           310           315           320
242 Ala Tyr Val Pro Ser Leu Ala Leu Ser Thr Leu Asn Ser Cys Val Asp
243           325           330           335
244 Pro Phe Ile Tyr Tyr Tyr Val Ser Ala Glu Phe Arg Asp Lys Val Arg
245           340           345           350
246 Ala Gly Leu Phe Gln Arg Ser Pro Gly Asp Thr Val Ala Ser Lys Ala
247           355           360           365
248 Ser Ala Glu Gly Gly Ser Arg Gly Met Gly Thr His Ser Ser Leu Leu
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250 Gln

251 385

253 <210> SEQ ID NO: 3

254 <211> LENGTH: 1155

255 <212> TYPE: DNA

256 <213> ORGANISM: Artificial Sequence

258 <220> FEATURE:

259 <223> OTHER INFORMATION: This degenerate nucleotide sequence encodes the  
 260 amino acid sequence of SEQ ID NO:2.

262 <221> NAME/KEY: variation

263 <222> LOCATION: (1)...(1155) /

264 <223> OTHER INFORMATION: N is any nucleotide.

266 <400> SEQUENCE: 3

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W--> 268 caracnccnw sngntayga ygarwsnggn wsnaacngng gngngayga ywsnacnccn      120
W--> 269 wsnathytn cngcncnmng nggntayccn ggncargtnt gygcnaayga ywsngayacn      180
W--> 270 ytngarytn cngaywsnws nmngcnytn ytnytnngnt gggtnccnac nmgnytngt      240
W--> 271 ccngcnytn ayggyntngt nytnngtn ggnytncng cnaayggyt ngcnytngtg      300
W--> 272 gtnytnngcna cncargcncc nmgnytnccn wsnaacnatg tnytnatgaa yytnngcnacn      360
W--> 273 gcngayytny tnytnngcny ngcnytnccn ccmgnathg cntaycayt nmngngncar      420
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W--> 275 tayggwnsng tnytnytnyt ngcngcngtn wsnytnngaym gntayytngc nytnngtnay      540
W--> 276 ccnytnmgng cnmngcnytn nmngngnmgn mgnytnngcny tnggnytnng yatggcngcn      600
W--> 277 tggynatg gngcngcnytn ngcnytnccn ytnacnytn armgncarac nttymgnytn      660
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W--> 279 tggcargcng cnttyacntg yytnngcnytn ytnngntgyt tytnccnytn nytnngcnatg      780
W--> 280 ytnytnngyt ayggngcnac nytnacayacn ytnngcngcnw sngngnmngm ntayggncay      840
W--> 281 gcnymngny tncngcngt ngtnytnngcn wngcngtng cnttytygt nccnwsnaay      900
W--> 282 ytnytnytny tnytnayta ywsngayccn wsncnwsng cntggggnaa yytnaygg      960
W--> 283 gcntaygtnc cnwsnytnngc nytnwsnacn ytnaaywsnt gygtngaycc nttyathtay      1020
W--> 284 taytaygtw sngcngartt ymgngayaar gtnmgngcng gnytnntyca rmgnwnsccn      1080
W--> 285 ggngayacng tngcnwsnaa rgnwnsngcn gargngngw sngngngnat gggncncay      1140

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VERIFICATION SUMMARY                      DATE: 03/05/2001  
PATENT APPLICATION: US/09/371,333A        TIME: 14:42:26

Input Set : A:\Pto.vsk  
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L:267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3